

	10	20	30	40	50	
C1QC_HUMAN	MDVGPSSLP	HLGLKLLLLLLLLL	ALRGQANT	-----		30
ACR3_HUMAN	MLLLGAVLLLL	LALPGHDQETTT	QGPGVLLPLPK	ACTGWMA	-----	41
HUZACRP2	MIPWVLLACAL	PCAADPLLGAFA	RRDFRKGSPQL	VCSLP	-----	39
	60	70	80	90	100	
C1QC_HUMAN	-----G	CYGIPGMPGL	PGAPGKDG	YDGLPGPKGE	PGIPAIPGIR	GP 71
ACR3_HUMAN	GIPGHPGHNG	APGRDGRDGT	PGEKGEKGD	PGLIGPKGD	IGETGVPGA	EGP 91
HUZACRP2	GPQGPPGPP	GAPGPSGMM	GRMGFPKDG	QDGHGDRG	DSGEEGPP	GRTGN 89
	110	120	130	140	150	
C1QC_HUMAN	KGQKGEPL	PGHPGKNG	PMGPPGMP	GVPGPMGIP	GEPEGEEGR	Y----- 114
ACR3_HUMAN	RGFPGIQ	GRKGEP	-----			104
HUZACRP2	RGKPGPKG	KAGAI	GRAGPRGP	KGVNGTPG	KHGTGPKK	GPKGKKGEPL 139
	160	170	180	190	200	
C1QC_HUMAN	----KQKFQ	SVFTVTRQTH	QPPAPNSL	IRFNAVL	TNPQGDYDT	STGKFTC 160
ACR3_HUMAN	--GEGAYV	YRSAFSV	GLETYVTI	PNMPIRFT	KIFYNQNH	DYGSTGKFHC 152
HUZACRP2	PCSCGSGH	TKSAFSV	AVTKSYPR	ERLPIKF	DKILMNEG	GHYNASSGKFVC 189
	210	220	230	240	250	
C1QC_HUMAN	KVPGLYYF	VYHAS-HTAN	LCVLLYRSG	---VKVVT	FCGHTSKTN	QVN--S 204
ACR3_HUMAN	NIPGLYYF	AYHITVYM	KDVKVSLE	FKK---DKA	MLFTYDQY	QENNVDQAS 198
HUZACRP2	GVPGIYYF	TYDITLANK	HLAIGLV--	HNGQYRI	RTFDANTG	-NHDVA--S 234
	260	270	280	290	300	
C1QC_HUMAN	GGVLLRLQ	VGEEVWLAV	NDYYDMVG	IQG----SD	SVFSGFLL	FPD----- 245
ACR3_HUMAN	GSVLLHLE	VGDQVWLQ	VYGEGERN	GLYAD-ND	NDSTFTG	FLLYHDTN--- 244
HUZACRP2	GSTILALK	QGDEVWLQ	IF-YSEQN	GLFYDPY	WTDSLFTG	FLLIYADQDDPN 283
C1QC_HUMAN	--					
ACR3_HUMAN	--					
HUZACRP2	EV	285				

Figure